STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/553,906β*
Source: *1 FWO*
Date Processed by STIC: *11/8/06*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
<u>Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:</u>

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/553,906 B_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
   Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
   prevent "wrapping."

2 ____Invalid Line Length   The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3 ____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
   Numbering   use **space characters**, instead.

4 ____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
   ensure your subsequent submission is saved in ASCII text.**

5 ____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
   each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
   residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
   "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
   previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
   the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
   Artificial or Unknown sequences.**

7 ____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
   (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   This sequence is intentionally skipped
   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
   (NEW RULES)   <210> sequence id number
   <400> sequence id number
   000

9 ____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
   (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
   Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
   is Artificial Sequence. (see item 11 below)

11 ____Use of <220>   Sequence(s) ____missing the <220> "Feature" and associated numeric identifiers and responses. Use
   of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
   Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
   explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
   Sequence Rules

12 ____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
   "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
   listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFWO

RAW SEQUENCE LISTING   DATE: 11/08/2006
PATENT APPLICATION: US/10/553,906B   TIME: 13:15:36

          Input Set : A:\PTO.RJ.txt
          Output Set: N:\CRF4\11082006\J553906B.raw

     3 <110> APPLICANT: Skanemejerier AB   *this is not the invention title*
     5 <120> TITLE OF INVENTION: (NEW ENZYME AND ITS USE)   *in official U.S.*
     7 <130> FILE REFERENCE: 75086   *application.*
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/553,906B   *(see p. 3)*
C--> 9 <141> CURRENT FILING DATE: 2005-10-21
     9 <150> PRIOR APPLICATION NUMBER: US 60/320,139   *Does Not Comply*
    10 <151> PRIOR FILING DATE: 2003-04-24   *Corrected Diskette Needed*
    12 <150> PRIOR APPLICATION NUMBER: US 60/481,598   *see*
    13 <151> PRIOR FILING DATE: 2003-11-05   *item 4 on*
    15 <160> NUMBER OF SEQ ID NOS: 18   *Erra Summary*
    17 <170> SOFTWARE: PatentIn version 3.2   *Sheet*

ERRORED SEQUENCES

   690 <210> SEQ ID NO: 18
   691 <211> LENGTH: 31
   692 <212> TYPE: DNA
   693 <213> ORGANISM: Unknown   *insufficient response - give source of genetic material*
   695 <220> FEATURE:
   696 <223> OTHER INFORMATION: (Artificial)   *same erra*   *(see item 11 on*
   698 <400> SEQUENCE: 18   *in seqs. 10-15,17*   *Erra*
   699 acgtcgactt accagcacca taacagccaa g   31   *Summary*
E--> 708 (1)   *Sheet)*
       delete

VERIFICATION SUMMARY   DATE: 11/08/2006
PATENT APPLICATION: **US/10/553,906B**   TIME: 13:15:37

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\11082006\J553906B.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:238 M:283 W: Missing Blank Line separator, <400> field identifier
L:401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:900
L:708 M:254 E: No. of Bases conflict, this line has no nucleotides.

3

AMENDMENTS TO THE SPECIFICATION:

On page 1, before line 1, please insert:

-- Title of the Invention--

On page 1, please amend line 1 as follows:

~~NEW ENZYME AND ITS USE~~ Human Alkaline Sphingomyelinase and use thereof

applicant must charge $120? response to this

On page 1, after line 1, please insert:

--Cross Reference to Related Applications

This application is a national stage application of International Application

PCT/SE2004/000628, filed April 23, 2004, designating the United States of America,

which claims the benefit of Provisional Patent Application No. 60/320,139, filed April

24, 2003 and Provisional Patent Application No. 60/481,598, filed November 5, 2003.

Field of the Invention--

Please replace the existing abstract with the following, which also follows on a

separate sheet at the conclusion of this submission:

-- An isolated human alkaline sphingomyelinase (Alk-Smase) or a variant thereof is

capable of hydrolysing sphingomyelin. Methods are provided for isolating human Alk-

Smase and for preparing human recombinant Alk-Smase. Further methods are

provided for the use of the enzyme for the treatment of colon cancer.--